

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:44:38 ; Search time 1165.71 Seconds
(without alignments)
3990.731 Million cell updates/sec

Title: US-09-424-705-1
Perfect score: 909
Sequence: 1 gaattcataagagagagaa.....atcaccatcactaatctaga 909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 110133 seqs, 2558875100 residues
2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_da1:
2: gb_da2:
3: gb_cm:
4: gb_ov:
5: gb_ph:
6: gb_pl1:
7: gb_pl2:
8: gb_pl1:
9: gb_pr2:
10: gb_pr3:
11: gb_ro:
12: gb_sy:
13: gb_un:
14: em_fun:
15: em_hum1:
16: em_hum2:
17: em_in:
18: em_cm:
19: em_or:
20: em_ov:
21: em_pat:
22: em_ph:
23: em_pl:
24: em_ro:
25: em_sy:
26: em_sy:
27: em_un:
28: em_vl:
29: gb_ba3:
30: gb_in1:
31: gb_in2:
32: gb_in3:
33: gb_pl3:
34: gb_pr4:
35: em_ba1:
36: em_ba2:
37: em_htg1:
38: em_htg2:
39: em_htg3:
40: em_htg4:
41: em_htg5:
42: em_htg6:
43: em_htg7:
44: em_htg8:
45: em_htg9:
46: em_htg10:
47: em_hum3:
48: em_hum4:
49: em_hum5:
50: em_hum6:
51: gb_pr5:
52: gb_pr6:
53: gb_pr7:
54: gb_htg1:
55: gb_htg2:
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73: gb_htg20:
74: gb_htg21:
75: gb_htg22:
76: gb_htg23:
77: gb_sts1:
78: gb_sts2:
79: gb_vl1:
80: gb_vl2:
81: gb_pat1:
82: gb_pat2:
83: em_htg0:
84: gb_htg24:
85: gb_pr8:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625.4	68.8	1653	13 AX011208	AX011208 Sequence
2	622.6	68.5	1698	13 AX011206	AX011206 Sequence
3	613.4	67.5	1611	51 AX014270	AX014270 Sequence
4	569	62.6	3991	12 ASY12778	Y12778 Artificial
5	527.4	58.0	1797	82 I84705	I84705 Sequence 2
6	515.2	56.7	810	81 A45006	A45006 Sequence 1
7	504	55.4	738	11 AF074900	AF074900 Mus muscu
8	499.8	55.0	717	11 AF025535	AF025535 Mus muscu
9	496	54.6	723	11 AF035617	AF035617 Mus muscu
10	490	53.9	1815	12 AF189283	AF189283 Synthetic
11	489.8	53.9	735	12 AF162710	AF162710 Synthetic
12	489	53.8	843	81 A83223	A83223 Sequence 43
13	488.6	53.8	1254	12 AF148718	AF148718 Synthetic
14	487.6	53.6	726	81 A46598	A46598 Sequence 29
15	485.6	53.4	738	81 A46592	A46592 Sequence 23
16	485.6	53.4	738	81 AR063194	AR063194 Sequence
17	483.8	53.2	726	81 A46594	A46594 Sequence 25
18	483.8	53.2	726	81 AR063195	AR063195 Sequence
19	483	53.1	3970	12 ASY14585	Y14585 Artificial
20	479.6	52.8	732	81 A46588	A46588 Sequence 19
21	479.6	52.8	732	81 A46600	A46600 Sequence 31

22	479.6	52.8	732	81	AR063192
23	473	52.0	732	81	EL13410
24	471.6	51.9	732	81	A46590
25	471.6	51.9	732	81	AR053193
26	470.2	51.7	314384	64	AC025152
27	470	51.7	235717	69	AC068947
28	469.8	51.7	723	12	AF169027
29	468.4	51.5	726	81	A46596
30	468.4	51.5	726	81	AR063196
31	468.4	51.5	2364	81	EL13412
32	465.2	51.2	2478	12	AX019954
33	464.2	51.1	217102	71	AC078911
34	461	50.7	725	81	A97142
35	457.4	50.3	4363	12	SCFV18290
36	456.2	50.2	4864	12	ASV14584
37	455.8	50.1	1679	81	AR054409
38	454	49.9	798	11	AF000955
39	452.2	49.7	726	11	MM020617
40	442.4	48.7	696	11	AF003721
41	442.2	48.6	1998	81	A83330
42	443.6	47.7	684	11	AF003720
43	430.6	47.4	696	11	AF003724
44	424.4	46.7	678	11	AF003714
45	423.2	46.6	702	11	AF003708
46					
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99					
100					

ALIGNMENTS

RESULT 1			
AX011208	AX011208	1653 bp	DNA
LOCUS			
DEFINITION	Sequence 3 from Patent WO9557150.		
ACCESSION	AX011208		
VERSION	AX011208.1	GI:9997788	
			06-SEP-2000

SOURCE ORGANISM	REFERENCE
unidentified.	1 (bases 1 to 1653)
unidentified	Kipriyanov, S. and Little, M.
unclassified.	Multivalent antibody constructs
	Patent: WO 9957150-A 11-NOV-1999;

FEATURES	Location/Qualifiers
source	1. .1653
	/organism="unidentified"
	/db_xref="taxon:32644"
CDS	28. .1647

BASE COUNT	432 a	429 c	424 g	368 t
ORIGIN				

Query Match	68.8%;	Score 625.4;	DB 13;	Length 1653;
Best Local Similarity	85.9%;	Pred. No. 4.5e-181;		
Matches: 733; Conservative	0;	Mismatches 81;	Indels 39;	Gaps 2.

Db	825	GGCCGCTGTGTGGCCACGGTTCGAGGTGCAGGTGCAGCAGTGTGGGGGTGAGCTGTGAG	884
Oy	132	acctggggccctcagtgaaagatgctcgtcaaggctctctgtctacaccttaactagttaac	191
Db	885	GCCTGGGTCTCATGTGAAAGTTTCGCAAGGCTTGTGGCTATTGCATTCAGTAGCTACTG	944
Oy	192	gatcactgggttaaaagaagggccctgtgaacaggtctgtgaatggatctgatacatatccc	251
Db	945	GATGACTGTGGGTGAGCAGAGAGGCGCTGGACGGTCTGTGAGTGGATTGGACAGATTTGGCC	1004
Oy	252	tagccgttggttatactaaattacaatcaagaagttcaagaaaggcccaatctgtactacaga	311
Db	1005	TGGAGATGGGTATCTTAACTAACATGAGAAAGTTCAAGGGCTTAAGGCACTCTGACGCGA	1064
Oy	312	caaatctcccaagcaacagctacatatgtcaactgtgaacagccctgacatcttgagactctgagt	371
Db	1065	CGAATCTCCAGCAGACACCTCAATGCACTCAGACACCTCAGATCTGAGAGACTCGCGCT	1124
Oy	372	ctattactgtgcaagatatata-----tgatgatcatlaagccttgacta	416
Db	1125	CTATTCTGTGCAAGAGGGAGACTACGACGGTAGGCGCTTATTCTATTGCTATGACTA	1184
Oy	417	ctgggggccaagggcaacacctctcaagctctccctccgaagcaaaacaccccaagcttgaaga	476
Db	1185	CTGGGGGTCAAGGAACCTCACTGACCGCTCTCTTAGCCAAAACACCACCCAGCTTG-----	1240
Oy	477	aggtgaatttbcagaagcaagcgtatagatcgtgtctcaactcagtlctcagaacatcagtc	536
Db	1241	-----GCGGTATATCGGCTCATCTCAGTCTCCAGCATCATATGTC	1280
Oy	537	tgcactcccaagggagagaggttcaacatgacatgacgtccagttgcacatcaatgtgaagttaac	596
Db	1281	TGCATCTCCAGGGAGAGAGTTCACCAATGACCTGCACTGCACTCAAGTGAAGTTACAT	1340
Oy	597	gaacttggctaccagaagaagaagtcacagacacctcccccacaaagaatggatctatgacacatccaa	656
Db	1341	GAACTGGTACAGCAGAAAGTCAGAGCACTCCCCCAAAAGATGATTTATGACACATCCAA	1400
Oy	657	actggtctctggagatccctctcaacttaattcaaggagcagttggtcttggaactcttaactct	716
Db	1401	ACTGGCTTCTTGAGATCCCTCTCTCACTTCAAGGGCACTGGGTCTGGGACCTCTTACTCTCT	1460
Oy	717	cacatcaagcgcatagtgaagcttgaagaatgctgtcaccttcttaactgcacagcagttgagtag	776
Db	1461	CACATATCAGCGGCAATGGAAGCTGAAGTGTGCACTTATTACTGCGACAGCACTGGAGTAG	1520
Oy	777	taaccaccatcaagtcgtgctcgggagacaaagttgaaataaaacccgggtctgataactctgacc	836
Db	1521	TAAACCATTCACGTTTCGGCTCGGGGAGCAAAAGTTGGAATAAACCGGGCTGATATGCAACC	1580
Oy	837	aactggatccgaanaaagaagtgtatccagaagaagacctaactacatatcaactacacaa	896
Db	1581	AACGTGATCCGACAAACAAAGCTGATCTTCAGAGAAGACCTTAATCTCAGATCAACCATCACCA	1640
Oy	897	tcactaatctaga	909
Db	1641	TCACTAATCTAGA	1653

RESULT	2		
AX011206			
LOCUS	AX011206	1698 bp	DNA
DEFINITION	Sequence 1 from Patent WO957150.		
ACCESSION	AX011206		
VERSION	AX011206.1	GI:9997786	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1698)		
AUTHORS	Kipriyanov, S. and Little, M.		
TITLE	Multivalent antibody constructs		

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:10:13 ; Search time 559.48 Seconds
(without alignments)
11385.226 Million cell updates/sec

Title: US-09-424-705-1
Perfect score: 969
Sequence: 1 gaattcataaagagagaa.....atcacatcactaatctaga 909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
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 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	292.6	32.2	472 106	BE289692 601088922
2	287.8	31.7	406 139	BE289692 601088922
3	283	31.1	396 10	AA691311 v814f01.r
4	259.6	28.6	413 110	BE289692 601088922
5	258.8	28.5	739 106	BE289692 601088922
6	257.8	28.4	644 106	BE289692 601088922
7	254	27.9	358 136	BE289692 601088922
8	253	27.8	464 107	BE289692 601088922
9	251.8	27.7	620 107	BE289692 601088922
10	250.4	27.5	401 139	BE289692 601088922
11	249.2	27.4	507 139	BE289692 601088922
12	247.6	27.2	432 159	BE289692 601088922
13	247.6	27.2	1057 106	BE289692 601088922
14	243.6	26.8	408 139	BE289692 601088922
15	236.8	26.1	473 106	BE289692 601088922
16	233.6	25.7	596 106	BE289692 601088922
17	232.4	25.6	554 174	BE289692 601088922
18	232	25.5	567 106	BE289692 601088922
19	231	25.4	911 106	BE289692 601088922
20	227	25.0	512 139	BE289692 601088922
21	225.6	24.8	379 96	BE289692 601088922
22	224	24.6	439 104	BE289692 601088922
23	222.2	24.4	634 107	BE289692 601088922
24	220.4	24.2	601 172	AA2447391
25	215.8	23.7	344 9	AA592800
26	214.6	23.6	443 139	BE289692 601088922
27	209.2	23.0	448 90	BE289692 601088922
28	207.2	22.8	380 23	AA641928
29	206.4	22.7	549 136	BE289692 601088922
30	204.2	22.5	427 136	BE289692 601088922
31	200.6	22.0	310 17	AA180569
32	200	22.0	398 87	AA229526
33	198	21.8	688 172	AA2399191
34	197.6	21.7	293 30	AA052316
35	196.6	21.6	477 90	AA03686
36	195.4	21.5	517 90	AA08270
37	192.8	21.2	485 90	AA03940
38	189.6	20.9	542 90	AA05977
39	188.6	20.7	510 90	AA03806
40	188.4	20.7	488 90	AA03591
41	187.2	20.6	457 90	AA05627
42	185.2	20.4	294 14	AA1007196
43	183.8	20.2	419 90	AA042189
44	183.8	20.2	639 107	BE371136
45	183.6	20.2	460 90	AA06939

ALIGNMENTS

RESULT 1
 BE289692
 LOCUS
 DEFINITION 601088922F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:3483797 5',
 mRNA sequence.
 ACCESSION BE289692
 VERSION BE289692.1 GI:9170234
 KEYWORDS
 SOURCE house mouse.

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:54:48 ; Search time 79.87 Seconds
(without alignments)
4275.415 Million cell updates/sec

Title: US-09-424-705-1

Perfect score: 909
Sequence: 1 gattcatctaagagagagaa.....atccacatcataatcata 909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

N_Geneseq_36.*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	710.4	78.2	1794	19	Mouse bispecific a
2	644	70.8	898	19	Mouse OKT3 variant
3	625.4	68.8	1653	21	Fv-antibody constr
4	622.6	68.5	1698	21	Fv-antibody constr
5	613.4	67.5	1611	21	Nucleotide sequen
6	527.4	58.0	1797	19	Fusion gene sequen
7	527.4	58.0	1797	21	Recombinant DNA en
8	515.2	56.7	810	16	MFE-23 antibody co
9	513	56.4	1797	20	Vm-VI-linker-Pk40
10	494.2	54.4	717	18	Single chain anti-
11	489	53.8	843	20	Fusion protein PIC
12	488.4	53.7	1175	18	Single chain anti-

13	486	53.5	726	16	T04025	Anti-EGFR single c
14	485.6	53.4	738	16	T04022	Anti-EGFR single c
15	483.8	53.2	726	16	T04023	Anti-EGFR single c
16	479.6	52.8	732	16	T04020	Anti-EGFR single c
17	479.6	52.8	732	16	T04026	Anti-EGFR single c
18	473	52.0	732	19	V23579	Firefly luciferase
19	471.6	51.9	732	16	T04021	Anti-EGFR single c
20	468.4	51.5	726	16	T04024	Anti-EGFR single c
21	468.4	51.5	2364	19	V23580	Antibody-Firefly 1
22	465.2	51.2	2478	20	X86614	cDNA encoding an a
23	461	50.7	725	20	V72075	Mouse scfv DNA fra
24	458.6	50.5	807	21	Z28963	Anti-Hepatitis B s
25	455.8	50.1	1679	18	T58130	Single chain anti-
26	455.8	50.1	1679	20	X08176	H22-anti-CEA antib
27	446	49.1	894	20	X33931	HBV specific singl
28	442.2	48.6	1998	20	V72075	Fusion protein (80
29	412.8	45.4	800	21	A08034	Antibody fragment
30	412.6	45.4	843	20	X01657	Anti-B7.1/B7.2 bis
31	400.2	44.0	828	20	X01661	Anti-B7.1/anti-b7.
32	397.2	43.7	831	15	O62957	Anti-Influenza N10
33	393.8	43.3	883	20	X58688	Monoclonal antibod
34	391.4	43.1	6115	18	T63235	Eukaryotic express
35	391	43.0	870	13	Q36982	Ox VH-hinge-VL ins
36	387.6	42.6	843	19	V73323	Human scFvCD19 DNA
37	387.6	42.6	1452	19	V73324	Chimeric CD19/CTCR
38	387	42.6	813	20	X56753	Mouse scfv fragmen
39	385	42.4	951	20	Z20266	cDNA coding single
40	382	42.0	840	21	A08033	Antibody fragment
41	381.4	42.0	837	20	X08492	scFv comprising he
42	379.8	41.8	720	19	V54790	Fusion protein PIC
43	379.8	41.8	864	20	V72072	Human CD30 binding
44	378.8	41.7	744	19	V11399	Antibody 4H5 L cha
45	377.6	41.5	925	21	Z58664	

ALIGNMENTS

RESULT 1	
V73337	standard; DNA: 1794 BP.
ID	V73337
AC	V73337
XX	
XX	26-FEB-1999 (first entry)
DT	
DE	Mouse bispecific antibody construct variant OKT3/anti-CD19 DNA.
XX	
KW	OKT3; monoclonal antibody; Mab; point mutation; transplant rejection;
KW	organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19;
KW	anti-CD3; ss.
XX	
OS	Mus sp.
OS	Synthetic.
FH	
FT	Key
FT	28..894
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "mutant OKT3 with anti-CD19 insert"
FT	922..1788
FT	/*tag= b
FT	/product= "mutant OKT3 with anti-CD3 insert"
DE19721700-Cl.	
XX	
PD	19-NOV-1998.
XX	
PF	23-MAY-1997; 97DE-1021700.
XX	
PR	23-MAY-1997; 97DE-1021700.
XX	
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX	

PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI: 1998-596150/51.
 DR P-PSDB: W82317, W82482.
 XX
 PT Monoclonal antibody OKT3 with point-mutation - where cysteine is
 replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 XX
 PS Disclosure; Fig 3; 8pp; German.
 CC This sequence encodes a monoclonal antibody (MAb) diabyody derived from
 CC OKT3 with a point-mutation where Cys at position H100A is replaced with
 CC another polar amino acid, in this example Ser. The diabyody encodes two
 CC OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3
 CC activity. The MAb is used in lowering or eliminating the transplant
 CC rejection in an organ recipient and for diagnostic methods for tumours
 CC and tumour therapy.
 CC
 XX
 XX Sequence 1794 BP; 480 A; 468 C; 450 G; 396 T; 0 other;
 XX
 Query Match 78.2%; Score 710.4; DB 19; Length 1794;
 Best Local Similarity 88.1%; Pred. No. 3.4e-188;
 Matches 812; Conservative 0; Mismatches 71; Indels 39; Gaps 2;
 QY 3 attcattaaaggagagaattacatgaatactatgtctcagcagcgcgtgctt 62
 Db 897 attcattaaaggagagaattacatgaatactatgtctcagcagcgcgtgctt 956
 QY 63 gctgtcgtcgtcagcgtcagccgcgcagtgccagtgctgacagcagcttgaggctga 122
 Db 957 gctgtcgtcgtcagcgtcagccgcgcagtgccagtgctgacagcagcttgaggctga 1016
 QY 123 actggaagacactggcgctcagtgagatgtcctgcaagctctcgtcctacacttac 182
 Db 1017 gctgtgagagccctggctcctcagtgagatgtcctgcaagctctcgtcctacacttac 1076
 QY 183 taggtacaagatgacacgtggtaaaacagagccctggacaggtctcgtgagatgagta 242
 Db 1077 taggtacaagatgacacgtggtaaaacagagccctggacaggtctcgtgagatgagta 1156
 QY 243 catlaactcgtccgtgtgtatlaactaactaactgaagaagtcagacaaagccacat 302
 Db 1137 gatttgccttgagatgtgtactaactaactgaagaagtcagacaaagccacat 1196
 QY 303 gactacagacaaatccctccagacagcctatactgaactgacagcctgacatctgagga 362
 Db 1197 gactcgcagacaaatccctccagacagcctatactgaactgacagcctgacatctgagga 1256
 QY 363 ctctcagctcattactgttgaagatata-----tgatgattcattacag 407
 Db 1257 ctctcagctcattactgttgaagatata-----tgatgattcattacag 1316
 QY 408 ccttgaactatggggcagacagccactctcagactcctccacagccaaacaaacccca 467
 Db 1317 tatggaactatggggcagacagccactctcagactcctccacagccaaacaaacccca 1376
 QY 468 gcttgaagaaggtgaattttcagaagcagcgtatagatcgtgtcactcagctcagc 527
 Db 1377 gcttg-----gcgtgatatcgtgtcactcagctcagc 1412
 QY 528 aatcatgtctgcattctcagagggaaggttcacatgacacgtcagtgccacataaggt 587
 Db 1413 aatcatgtctgcattctcagagggaaggttcacatgacacgtcagtgccacataaggt 1472
 QY 588 aagttaatatgactgtacacaggaagtcagcagcactcccccacaaagatgattatga 647
 Db 1473 aagttaatatgactgtacacaggaagtcagcagcactcccccacaaagatgattatga 1552
 QY 648 cacatccaactggtctcgtgagtcctgtcactcactcaggggagctgggtctggagctc 707
 Db 1533 cacatccaactggtctcgtgagtcctgtcactcactcaggggagctgggtctggagctc 1592

QY 708 ttactctcacaatcagcgcatggaagctgaagatgctccacttaactgcacga 767
 Db 1593 ttactctcacaatcagcgcatggaagctgaagatgctccacttaactgcacga 1652
 QY 768 gtggaagtagtaaccatcactacgttcgctcggggacaaagttggaataaacgggctga 827
 Db 1653 gtggaagtagtaaccatcactacgttcgctcggggacaaagttggaataaacgggctga 1712
 QY 828 tactggcaccactgataccggaacaaagctgattcagaagaagacctaactacatca 887
 Db 1713 tactggcaccactgataccggaacaaagctgattcagaagaagacctaactacatca 1772
 QY 888 ccataccatcactaactaga 909
 Db 1773 ccataccatcactaactaga 1794
 RESULT 2
 V73335
 ID V73335 standard; DNA; 898 BP.
 XX
 AC V73335;
 XX
 DT 26-FEB-1999 (first entry)
 XX
 DE Mouse OKT3 variant antibody DNA.
 XX
 KW OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; ss.
 OS Mus sp.
 OS Synthetic.
 XX
 PN DE19721700-Cl.
 XX
 PD 19-NOV-1998.
 XX
 PF 23-MAY-1997; 97DE-1021700.
 XX
 PR 23-MAY-1997; 97DE-1021700.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Kipriyanov S, Little M, Moldenhauer G;
 DR WPI: 1998-596150/51.
 DR P-PSDB: W82316.
 XX
 PT Monoclonal antibody OKT3 with point-mutation - where cysteine is
 replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 XX
 PS Claim 3; Fig 2; 8pp; German.
 CC This sequence encodes a monoclonal antibody (MAb) derived from OKT3 with
 CC a point-mutation where Cys at position H100A is replaced with another
 CC polar amino acid, in this example Ser. The MAb is used in lowering or
 CC eliminating the transplant rejection in an organ recipient, and for
 CC diagnostic methods for tumours and tumour therapy.
 CC
 XX
 SO Sequence 898 BP; 245 A; 236 C; 217 G; 200 T; 0 other;
 XX
 Query Match 70.8%; Score 644; DB 19; Length 898;
 Best Local Similarity 83.8%; Pred. No. 7.3e-170;
 Matches 769; Conservative 0; Mismatches 110; Indels 39; Gaps 2;
 QY 1 gaattcattaaaggaggaataatcaatgaatactatgctcagcagcgcgtggc 60
 Db 1 gaattcattaaaggaggaataatcaatgaatactatgctcagcagcgcgtggc 60
 QY 61 ttgtgtcgtcagcagctcagcgcatggtgcaggtgacagctgcagcagctggggt 120

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Db      61  ttgctgcgtcgcgcagctcagccagccatgagcagcgtcgcagcagctcgggct 120
Qy      121  gaactgggaagaactcgggctcagtgagaagtgtctcgaaggtctcgtctacacctt 180
Db      121  gaactgggaagaactcgggctcagtgagaagtgtctcgaaggtctcgtctacacctt 180
Qy      181  actagtgacagatgagcacttggttaaacagagagcctgagcagcgtctggaattgga 240
Db      181  actagtgacagatgagcacttggttaaacagagagcctgagcagcgtctggaattgga 240
Qy      241  tacatcaccctcagcgtgtgtatatactaatcacaatcagaaggtlcaagagacagccaca 300
Db      241  tacatcaccctcagcgtgtgtatatactaatcacaatcagaaggtlcaagagacagccaca 300
Qy      301  ttgactacagaacaatctctcagcagcagcctacatgacagcagcgtgagcctgacatcag 360
Db      301  ttgactacagaacaatctctcagcagcagcctacatgacagcagcgtgagcctgacatcag 360
Qy      361  gactcgcagctatctactgtgcagaagatatatgatagtatcattacagcctgactcag 420
Db      361  gactcgcagctatctactgtgcagaagatatatgatagtatcattacagcctgactcag 420
Qy      421  ggccaagggacacactctacagctctcagccaaacaaacacacccaagcttgaagaagt 480
Db      421  ggccaagggacacactctacagctctcagccaaacaaacacacccaagcttgaagaagt 480
Qy      481  gaatttcagaagaacagcgtatgatatgtgtcactcactcgtctccagcagcattgtctgca 540
Db      473  -----ggcggtatatactgtctcaccacccaacccaagctcttctgtgtg 516
Qy      541  tctcagggagagaagtgacacatgacatgacagctgcagctgcagctcaagctga----- 588
Db      517  tctctagggcagagggccacacatctctcagcagcagccaaaggttgatgatatgagtgt 576
Qy      589  ---agttacatgaaactgtgtaccagcagaagtcagggcaccctccccaagaagtgtattat 645
Db      577  gatagttattggaactgtgtaccacacagattccagagcagcagcacaacacactcctcatat 636
Qy      646  gacacatccaactcgtcgtcgtgaggtccctcgtcactcactcaggggaggggtctggagcc 705
Db      637  gatcattccaactcagttctcgtgaggtccacacaggtttagttggaggtcctggagca 696
Qy      706  tctactctccacacatcagcagcgtgaggtgaggtgaggtgtcgtcacttatactacagcag 765
Db      697  gactcaccctcaacatcaccctcgtgagagaggtgaggtgtcgtcacttatactacagcag 756
Qy      766  cagtggagtagtaaccatcactcaggttcggtcgggagacaaagtgtgaaataaacccgggct 825
Db      757  caaagtactcagagatccgttgagcgttcgtgtgagagcaccagcgtggaatacaaacgggct 816
Qy      826  gatctgcacccaactgtagtcggaacaaagtgtatctcagaagaagagactaacatcaat 885
Db      817  gatctgcgagcgcgtgagtcggaacaaagtgtatctcagaagaagactaacatcaat 876
Qy      886  caccatcaccatcaactaa 903
Db      877  caccatcaccatcaactaa 894

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RESULT 3
ID      243432
XX      243432 standard; DNA; 1653 BP.
AC      243432;
XX      18-FEB-2000 (first entry)
DT      Fv-antibody construct containing antibody 9E10 epitope DNA.
XX      Fv-antibody construct containing antibody 9E10 epitope DNA.
KM      Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
XX      diagnosis; therapy; disease; ss.
XX

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OS      Synthetic.
XX      DEL9819846-A1.
XX      11-NOV-1999.
XX      05-MAY-1998; 98DE-1019846.
XX      05-MAY-1998; 98DE-1019846.
XX      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX      Little M, Kipriyanov S;
XX      WPI: 2000-024472/03.
XX      Multivalent Fv-antibody constructs with at least four variable domains
XX      connected by 1, 2 and 3 peptide linkers
XX      Example 1; Fig 6; 14pp; German.
XX      This invention describes a novel multivalent Fv-antibody construct with
XX      at least four variable domains that are connected to one another by 1,
XX      2 and 3 peptide linkers. The construct has antiviral, antibacterial
XX      and cytostatic activity. The multivalent Fv-antibody constructs are
XX      useful for the diagnosis and/or therapy of disease, especially viral,
XX      bacterial or tumor diseases. The multivalent Fv-antibody constructs have
XX      increased stability when in the form of a single chain dimer. This
XX      sequence encodes a tetravalent Fv antibody construct composed of the
XX      antibody 9E10 epitope in expression plasmid pDSC19-SL
XX      Sequence 1653 BP; 432 A; 429 C; 424 G; 368 T; 0 other;

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Query Match      68.8%; Score 625.4; DB 21; Length 1653;
Best Local Similarity 85.9%; Pred. NO. 1.5e-164;
Matches 733; Conservative 0; Mismatches 81; Indels 39; Gaps 2;

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Qy      72  ggcaactcagccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 131
Db      825  ggccgctgtgtgcccagggctcagagtgagcagcagcagcagcagcagcagcagcagcagcagc 884
Qy      132  acctgggctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 191
Db      885  gactggtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 944
Qy      192  gatcactgggttaaacagagagcgtgcagcagcagcagcagcagcagcagcagcagcagcagc 251
Db      945  gatgaactgggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1004
Qy      252  tagccgtgtgtatatactaatcacaagaggttcaagagcagcagcagcagcagcagcagcagcagc 311
Db      1005  tggagatggtgatactaatcacaagaggttcaagagcagcagcagcagcagcagcagcagcagcagc 1064
Qy      312  caaactcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 371
Db      1065  cgaatccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1124
Qy      372  ctattactgtcagagatata-----tagatatactacagccttgacta 416
Db      1125  ctattctgtgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1184
Qy      417  ctggggccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 476
Db      1185  ctgggggtcaagaaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1240
Qy      477  aggtgaatttcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 536
Db      1241  -----ggcggtatatactgtcactcagcagcagcagcagcagcagcagcagcagcagcagc 1280
Qy      537  tgcatctcagagggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 596
Db      1281  tgcatctcagagggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1340

```

QY 597 gaactgtaccagcagaagtcagccaccctcccaaaagatgattttagacacatccaa 656
 |||||||
 Db 1341 gaactgtaccagcagaagtcagccaccctcccaaaagatgattttagacacatccaa 1400
 QY 657 actgtgtcttgagtgccctgtcacttcacccaaggagtggtcttgagaccttactct 716
 |||||||
 Db 1401 actgtgtcttgagtgccctgtcacttcacccaaggagtggtcttgagaccttactct 1460
 QY 717 cacatcagcagcagtgagtgatgagtgctgcacacttattacggccagcgttgagtag 776
 |||||||
 Db 1461 cacatcagcagcagtgagtgatgagtgctgcacacttattacggccagcgttgagtag 1520
 QY 777 taaccattccgtctcgctcgaggagacaagtgtgaaataaccgggtctgactgaccc 836
 |||||||
 Db 1521 taaccattccgtctcgctcgaggagacaagtgtgaaataaccgggtctgactgaccc 1580
 QY 837 aactgagtcgcgaacaaagctgacttcagaagaagaccctaaactacacacacacac 896
 |||||||
 Db 1581 aactgagtcgcgaacaaagctgacttcagaagaagaccctaaactacacacacacac 1640
 QY 897 tcaactatctaga 909
 |||||||
 Db 1641 tcaactatctaga 1653

RESULT 4

243431
 ID 243431 standard; DNA; 1698 BP.

AC 243431;

DT 18-FEB-2000 (first entry)

DE Fv-antibody construct containing antibody 9E10 epitope DNA.

XX Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;

KM diagnosis; therapy; disease; ss.

OS Synthetic.

XX DE19819846-A1.

PN 11-NOV-1999.

PD 05-MAY-1998; 98DE-1019846.

PE 05-MAY-1998; 98DE-1019846.

PF 05-MAY-1998; 98DE-1019846.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Little M. Kipriyanov S;

DR WPI: 2000-024472/03.

DR P-PSDB; Y50822.

XX Multivalent Fv-antibody constructs with at least four variable domains

XX connected by 1, 2 and 3 peptide linkers

XX Example 1; Fig 5; 14pp; German.

XX This invention describes a novel multivalent Fv-antibody construct with

XX at least four variable domains that are connected to one another by 1,

XX 2 and 3 peptide linkers. The construct has antiviral, antibacterial

XX and cytostatic activity. The multivalent Fv-antibody constructs are

XX useful for the diagnosis and/or therapy of disease, especially viral,

XX bacterial or tumor diseases. The multivalent Fv-antibody constructs have

XX increased stability when in the form of a single chain dimer. This

XX sequence encodes a bivalent Fv antibody construct composed of the

XX antibody 9E10 epitope in expression plasmid pDISC3x19-LL

XX Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 other;

Query Match 68.5%; Score 622.6; DB 21; Length 1698;
 Best Local Similarity 87.0%; Pred. No. 8.9e-164;
 Matches 723; Conservative 0; Mismatches 69; Indels 39; Gaps 2;

QY 94 caggtgcagctgcagcagctctgggctgtaactggcaaacctgggctcagtgaaagt 153
 |||||||
 Db 892 caggtgcagctgcagcagctctgggctgtaactgggctcagtgaaagt 951
 QY 154 tccgtgcaaggttttgctacacttactaggtacacagtgacgtgggttaacagagg 213
 |||||||
 Db 952 tccgtgcaaggttttgctacacttactaggtacacagtgacgtgggttaacagagg 1011
 QY 214 cctggacaggtctggaatgattgatacattacccctgacggtgtgataacat 273
 |||||||
 Db 1012 cctggacaggtctggaatgattgatacattacccctgacggtgtgataacat 1071
 QY 274 aatcaagaagtcaaggaacaaagccacattgactacagaacaaatccctcagcagctac 333
 |||||||
 Db 1072 aatgaaagtcaaggaacaaagccacattgactacagaacaaatccctcagcagctac 1131
 QY 334 atgcaactgagcagcctgacactctgagagactctgacttactctgtgcaagatata 392
 |||||||
 Db 1132 atgcaactgagcagcctgacactctgagagactctgacttactctgtgcaagatata 1191
 QY 393 -----tgatgactatcagccttgactactgagggcagcagcactctc 438
 |||||||
 Db 1192 actcagacgtgagcgttactatctactatgctatgtaactctggttcaagaaactcagtc 1251
 QY 439 acaactctcctcagcacaac 498
 |||||||
 Db 1252 acaactctcctcagcacaac 1287
 QY 499 gtagatagctggtcactcactcagcttccagcaatcatgltctgatactccagggaaagt 558
 |||||||
 Db 1288 gtagatagctggtcactcactcagcttccagcaatcatgltctgatactccagggaaagt 1347
 QY 559 accatgacctgagctgagcagctcaagtgaagtacatgtaactgtaaccagaaatga 618
 |||||||
 Db 1348 accatgacctgagctgagcagctcaagtgaagtacatgtaactgtaaccagaaatga 1407
 QY 619 ggcacctcccccacaaagatgattatgacacatccaaactggtctcgtgagctcgt 678
 |||||||
 Db 1408 ggcacctcccccacaaagatgattatgacacatccaaactggtctcgtgagctcgt 1467
 QY 679 cacttcaggagcagtggtgtcgggaaccttactctcacaatcagcggagtagaggt 738
 |||||||
 Db 1468 cacttcaggagcagtggtgtcgggaaccttactctcacaatcagcggagtagaggt 1527
 QY 739 gaagatgctgcacttattactgcagcagtgagtagtaaccatcagctcgtcgtg 798
 |||||||
 Db 1528 gaagatgctgcacttattactgcagcagtgagtagtaaccatcagctcgtcgtg 1587
 QY 799 gggacaaagtgtgaaataaacccggctgatactgcaccacactgataccgaaacagtg 858
 |||||||
 Db 1588 gggacaaagtgtgaaataaacccggctgatactgcaccacactgataccgaaacagtg 1647
 QY 859 atctcagaagaagacctaaactacatcacatcacatcacatcacatcacatcacat 909
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 Db 1648 atctcagaagaagacctaaactacatcacatcacatcacatcacatcacatcacat 1698

RESULT 5

230332
 ID 230332 standard; cDNA; 1611 BP.

AC 230332;

DT 11-FEB-2000 (first entry)

DE Nucleotide sequence of the bscCD19xCD3 antibody.

XX bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen;

KW antibody; autoimmune disease; cancer cell; ss.
 XX
 OS Chimeric - Pseudomonas.
 OS Chimeric - Mammalia.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1797
 FT misc_feature 1..352
 FT /tag= a
 FT /note= "encodes mature variable domain of the heavy chain"
 FT misc_feature 353..396
 FT /tag= c
 FT /note= "linker"
 FT misc_feature 397..714
 FT /tag= d
 FT /note= "encodes mature variable domain of the light chain"
 FT misc_feature 715..1797
 FT /tag= e
 FT /note= "encodes amino acids 253-613 of PE40"
 XX
 PN US5696237-A.
 PD 09-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-0463163.
 XX
 PR 21-APR-1989; 89US-0341361.
 PR 24-SEP-1986; 86US-0911227.
 PR 08-APR-1992; 92US-0865722.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Chaudhary VK, Fitzgerald D, Pastan IH, Queen CL;
 PI Waldmann TA;
 XX
 DR WPI: 1998-041352/04.
 DR P-PSDB: W37132.
 XX
 PT Antibody toxin fusion proteins - useful as immuno:toxin for
 PT treating, e.g. lymphocytes associated with auto:immune disease
 XX
 PS Disclosure; Columns 13-18; 20pp; English.
 XX
 CC The present sequence encodes a protein that is an example of a novel
 CC antibody-pseudomonas exotoxin (PE) fragment recombinant fusion protein.
 CC It is designated anti-Tac(Fv)-PE40. The present fusion gene encodes
 CC various domains of the heavy chain (the first 116 amino acids), a 15
 CC amino acid linker, VL-variable domain of the light chain (first 106 amino
 CC acids), and amino acids 253-613 of PE. This PE fragment possesses
 CC translocating and ADP-ribosylating activity. The fusion gene is cloned
 CC under the control of a T7 promoter linked to Shine-Delgarno region and
 CC initiation codon. The fusion protein selectively inhibits protein
 CC synthesis in cells expressing the interleukin-2 receptor. The
 CC antibody-PE40 fusion protein is used as an immunotoxin for killing
 CC cells bearing a receptor or antigen to which the antibody binds.
 CC e.g. lymphocytes associated with autoimmune diseases or cancer cells.
 XX
 SQ Sequence 1797 BP; 336 A; 598 C; 571 G; 292 T; 0 other;

Query Match 58.0%; Score 527.4; DB 19; Length 1797;
 Best Local Similarity 84.8%; Pred. NO. 2.7e-137;
 Matches 620; Conservative 0; Mismatches 96; Indels 15; Gaps 2;

QY 93 gcaagtcagctgacagctggtgggtgacagtcgcaagacgtggggtcctcagtgaaagt 152
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 3 gcaggtcagctgacagctggtgggtgacagtcgcaagacgtggggtcctcagtgaaagt 62
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 153 gtccctgcaaggtctctgtgctacaccttactagttacaagtcagtcagtgtaaacagag 212
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 63 gtccctgcaaggtctctgtgctacaccttactagttacaagtcagtcagtgtaaacagag 122
 QY 213 gcttggaagaggtcttggaatgattgataataatctctgacgtgtattactaatla 272
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 123 gcttggaagaggtcttggaatgattgataataatctctgacgtgtattactaatla 182
 QY 273 caatcagaagttcaaggaagggccacattgactacacaaatcctccacagacctta 332
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 183 caatcagaagttcaaggaagggccacattgactacacaaatcctccacagacctta 242
 QY 333 catgcaactgacagcctgacatctgagagctgcagctgtactactgtgcaagata 392
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 243 catgcaactgacagcctgacatctgagagctgcagctgtactactgtgcaagag 302
 QY 393 tgatgatcatctacagccttgactctggtgggcaagggccacacctctcagctcc 452
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 303 ggggg-----cttgactactgtgggcaaggaacacctctcagctccctccg 352
 QY 453 caaacaacacccaagcttgaagaagtgtaatttcagaagcacgctagatctgtgt 512
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 353 -----gagcggtgtgtcgtggcggtgtggcggtgtggcggtgtgtgtct 407
 QY 513 cactcagctccagcaatcatgtctgcatctccagggagagagtcacatgacctgcag 572
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 408 caccagctccagcaatcatgtctgcatctccagggagagagtcacatgacctgcag 467
 QY 573 tgcagctcgaagttaagtatacgaactgtgtaccagagagtcagcactcccca 632
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 468 tgcagctcgaagtatacgaactgtgtaccagagagtcagcactcccca 527
 QY 633 aagatgtattatcacaaatcgaactgtgtaccagagagtcagcactcccca 692
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 528 actctgtattatacacaatcgaactgtgtaccagagagtcagcactcccca 587
 QY 693 tgggtctgggaaccttactctcacaatcgaactgtgtaccagagagtcagcactcccca 752
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 588 tggatctgggaaccttactctcacaatcgaactgtgtaccagagagtcagcactcccca 647
 QY 753 ttattactgcagagtgagtagtaaccatcagctgtggcggtggagacaagttgga 812
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 648 ttattactgcagagtgagtagtaaccatcagctgtggcggtggagacaagttgga 707
 QY 813 aataaccggg 823
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 708 gtcgaaggcg 718

RESULT 7
 A10398
 ID A10398 standard; DNA; 1797 BP.
 XX
 AC A10398;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Recombinant DNA encoding anti-Tac(Fv)-PE40 fusion protein.
 XX
 KW Antibody-toxin fusion protein; single chain antibody; immunotoxin;
 KW Pseudomonas exotoxin; anti-Tac(Fv)-PE40; targeted delivery;
 KW Interleukin-2 receptor; IL-2; helper T-lymphocyte; autoimmune disease;
 KW Leukemia; ds.
 XX
 OS Chimeric - Pseudomonas sp.
 OS Chimeric - Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1797
 FT /tag= a
 FT /product= "Anti-Tac(Fv)-PE40 immunotoxin
 FT /note= "No stop codon given in the specification"
 FT /transl_except= (pos:1174..1176, aa:Asp)
 XX
 PN US6051405-A.

```

XX 18-APR-2000.
PD
XX 08-APR-1992; 92US-0865722.
PF
XX 21-APR-1989; 89US-0341361.
PR 24-SEP-1986; 86US-0911227.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Fitzgerald D, Chaudhary VK, Pastan IH, Queen CL, Waldmann TA;
XX
XX WPI: 2000-363771/31.
DR P-PSDB; Y87477.
XX
XX Construct encoding recombinant scFV-toxin fusion protein to selectively
XX kill cells bearing antigens or receptors comprises DNA segment -
XX
XX Claim 9; Columns 9-12; 14pp; English.
XX
XX This sequence represents DNA encoding a recombinant single chain
XX antibody fusion protein anti-Tac(Fv)-PE40, which comprises the heavy and
XX light chain variable regions (VH and VL) of an anti-Tac antibody and
XX residues 253-613 of Pseudomonas exotoxin (Pe). The anti-Tac single chain
XX antibody component of the immunotoxin binds to the p55 subunit (Tac
XX antigen) of the interleukin-2 (IL-2) receptor, which is present in large
XX amounts on helper T-lymphocytes. This enables the cytotoxic action of
XX PE40 to be targeted to these and other cell types which express the IL-2
XX receptor. The recombinant immunotoxin of the invention may be used to
XX treat a variety of autoimmune diseases, including graft-versus-host
XX disease, organ transplant rejection, type I diabetes, multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus and
XX myasthenia gravis. It may also be used in the treatment of leukaemia,
XX and may be used in vitro for the elimination of harmful cells from bone
XX marrow before transplant. Anti-Tac(Fv)-PE40 is more active on a molar
XX basis than anti-Tac antibody chemically conjugated to full-length PE
XX (anti-Tac-Pe) or to PE40 (anti-Tac-PE40).
XX
XX Sequence 1797 BP; 336 A; 599 C; 570 G; 292 T; 0 other:
XX
Query Match 58.0%; Score 527.4; DB 21; Length 1797;
Best Local Similarity 84.8%; Pred. No. 2.7e-137;
Matches 620; Conservative 0; Mismatches 96; Indels 15; Gaps 2;
XX
QY 93 gcaagtgacgtgcagcagctgtgggctgaactgacgaagacctgggctcagtaagat 152
D 3 gcaagtcacagctgcagcagctgtgggctgaactgacgaagacctgggctcagtaagat 62
QY 153 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacagag 212
D 63 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacagag 122
QY 213 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacatla 272
D 123 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacatla 182
QY 273 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacatla 332
D 183 gtcctgcaaggtctgtgctacaccttactagtagacacgaatgacatggttaaacatla 242
QY 333 catgcaactgacgacgctgacatctgagacatcagatcttactgtgcaagatla 392
D 243 catgcaactgacgacgctgacatctgagacatcagatcttactgtgcaagatla 302
QY 393 tgatgataactaacgaccttgacttgggccaaggaaccacactcaagatctcctcagc 452
D 303 tgatgataactaacgaccttgacttgggccaaggaaccacactcaagatctcctcagc 352
QY 453 caaacacaacacacgacgtgaaagagtgaaatttcagaagaagcgtagatatgttgt 512
D 353 caaacacaacacacgacgtgaaagagtgaaatttcagaagaagcgtagatatgttgt 407

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QY 513 cactcagctccagcaaatatgtctgcaltccagggagaaaggtcacatgacctgcag 572
D 408 caccagctctccagcaaatatgtctgcaltccagggagaaaggtcacatgacctgcag 467
QY 573 tgcagctccaagtgtgaatttaactgtgacagcagaagaagtgaagcactcccca 632
D 468 tgcagctccaagtgtgaatttaactgtgacagcagaagaagtgaagcactcccca 527
QY 633 aagatgatttaagcacatccaactgtgcttgcagtcctgcacttaaggggcag 692
D 528 actctgatttaacacacacacacacacacacacacacacacacacacacacacac 587
QY 693 tgggtctggaccttactctctcacaatcagcgagatgaggtgaagatgctgcac 752
D 588 tggatctggaccttactctctcacaatcagcgagatgaggtgaagatgctgcac 647
QY 753 ttattactgccaagctgagtagtaaccatcagctgctcggtggacaagtga 812
D 648 ttattactgccaagctgagtagtaaccatcagctgctcggtggacaagtga 707
QY 813 aataaccggg 823
D 708 gctcaaggcg 718
XX
XX RESULT 8
XX ID Q90663 standard; DNA: 810 BP.
XX AC Q90663;
XX DT 26-JAN-1996 (first entry)
XX DE MFE-23 antibody coding sequence.
XX KW Antibody; MFE-23; carcinoembryonic antigen; CEA; colorectal tumour;
XX therapy; diabody; ds.
XX OS Mus musculus.
XX
XX Key Location/Qualifiers
XX FT misc_feature 79..438
XX FT misc_feature /tag= a
XX FT misc_feature /note= "variable heavy chain"
XX FT misc_feature 439..483
XX FT misc_feature /tag= b
XX FT misc_feature /note= "linker region"
XX FT misc_feature 484..801
XX FT misc_feature /tag= c
XX FT misc_feature /note= "variable light chain"
XX
XX W09515341-A1.
XX PD 08-JUN-1995.
XX PF 05-DEC-1994; 94WO-GB02658.
XX PR 03-DEC-1993; 93GB-0024807.
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX PI Begent RHD, Chester KA, Hawkins RE;
XX WPI: 1995-215234/28.
XX DR P-PSDB; R75719.
XX
XX Antibody for carcinoembryonic antigen - for treatment and diagnosis
XX of colorectal cancer
XX
XX Claim 3; Page 48-49; 72pp; English.
XX
XX This sequence represents the coding sequence for the MFE-23 antibody.
XX

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Query Match	56.4%;	Score 513;	DB 20;	Length 1797;
Best Local Similarity	83.6%;	Pred. No. 2.8e-133;		
Matches 611; Conservative	0;	Mismatches 105;	Indels 15;	Gaps 2

OY	753	tatatctgcgcaagcagtgagttaataaccattcaagttcggtcccgaggacaaagtttga	812
Dd	648	ttatctactgcgccatcaaaggagtagtaccttacccactcagttcggttctgggacccaagctgga	707
OY	813	aataaacccggg	823
Dd	708	gctcgaagggcg	718

W09734634-A1.
25-SEP-1997.
20-MAR-1997; 97WO-US04427.
20-MAR-1996; 96US-0013703.
(SLOK) SLOAN KETTERING INST CANCER RES.
Cheung NV, Guo H, Larson SM, Rivlin K, Sadelain M;
NPI: 1997-479996/44.

Sequence 717 BP; 180 A; 181 C; 195 G; 159 T; 2 other;

Oy	94	caggtgcagcgtgcagcagctctgggctgaactggcaagacctgggctctcagtgaaatg	15
Db	1	caggtgaacactgcagcagctcaggaactgaactggctgggcttcagtgaaagata	60
Oy	154	tcctgcagagccttcctgcgtacaccttaactcgtgacagatgcacacttggttaaaacagag	213

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Db      61  ||||||| ||| ||| ||||| ||||| ||| |||||
      61  tcttgcagagctcttganaacaattccatgcaatcacacatgctggtgaagcagagc 120
Qy      214  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      214  cctggacaggtctgtgaatgattggtatcatatctctgcccgtgttatactaat 273
Db      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      121  catgaaagagccttgatggtatggtatattatcttaacaaatggtgtaacaaac 180
Qy      274  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      274  aatcagaagttcaagacagagccacattgactacagacaaatctccacagacac 333
Db      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      181  aagagaagttcaagacagagccacattgactacagacaaatctccacagacac 240
Qy      334  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      334  atgcaatgacagcctgacatgtaaggaactgacatctattactgtgcaagatat 393
Db      241  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      241  atgagagctccagcctgacatctgagatctctgacatcttactgtgcaagatat 300
Qy      394  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      394  gatgataatcacagcctgactactgtggtgagcagacacacactccacagacac 453
Db      301  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301  acggtccgtt-----ctgctactggtgccaaggaacacagcagcagcgtctcc 352
Qy      454  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      454  aaacaacacccaagcttgaagaagtgaaatttccagaagacagcgtatgatact 513
Db      353  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      353  ----gtgagagcggttcagggaggtggtgctctggtggtgagatcgacatcgag 408
Qy      514  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      514  actcagctccagcaatcatgctgcatctccagggaggaagatccacatgctgag 573
Db      409  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      409  actcagctccagcaatcatgctgcatctccagggaggaagatccacatgctgag 468
Qy      574  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      574  gccagcgaagtgtaagttatgtaactggtgacagcaggaagatcagacaccccaa 633
Db      469  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      469  ggcagctcaagataaagttacatgacatggtacacagcagaagcctgtacactcc 528
Qy      634  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      634  agatgattatgacacatccaactggtcttgaggtccctgctacattcaaggagc 693
Db      529  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      529  agatgattatgacacatccaactggtcttgaggtccctgctacattcaaggagc 588
Qy      694  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      694  ggtctgagacacttactctccacaaatcagcagatgagagctgtaagatgctgac 753
Db      589  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      589  ggtctgagacacttactctccacaaatcagcagatgagagctgtaagatgctgac 648
Qy      754  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      754  tattactgcccagatgagatgagtaaacatctcagctcgtcgtgggagacaagt 813
Db      649  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      649  tattactgcccagatgagatgagtaaacatctcagctcgtcgtgggagacaagt 708
Qy      814  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      814  ataaccgg 822
Db      709  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      709  ataaacgg 717

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XX      11  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      11  V72069 standard; DNA: 843 BP.
ID      V72069
AC      V72069:
XX      10-MAY-1999 (first entry)
DE      Fusion protein PIC1266/8061scfvtg/his DNA.
XX      Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
XX      prodng-converting enzyme; cell surface antigen; treatment; cancer;
XX      inflammation; rheumatoid arthritis; antibody; prodng therapy system; ss.
OS      Synthetic.
XX      WO9851787-A2.
XX      19-NOV-1998.
PD      05-MAY-1998; 98WO-GB01294.
PF      10-MAY-1997; 97GB-0009421.
PA      (ZENNE ) ZENNECA LTD.

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XX      Blakey DC, Emery SC;
PI      WPI: 1999-059700/05.
XX      DR      P-P-SDB: W82744.
XX      New gene construct expressing conjugate of targeting agent and
XX      PT      prodng-converting enzyme - useful for, e.g. targeted production of
XX      PT      cytotoxic drug in vivo, especially for treatment of cancer
XX      PS      Example 16; Page 84; 100pp; English.
XX      This sequence is a used in a method for obtaining a novel gene construct
XX      CC      (A) which expresses, in cells of a mammal, a conjugate (B) of a
XX      CC      cell-targeting group (I) and a heterologous prodng-converting enzyme
XX      CC      (II), and (B) is directed to leave the cell for selective localisation
XX      CC      at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
XX      CC      target site, then administration of (III) is used for targeted release of
XX      CC      cytotoxic drug, specifically for treating cancer but also inflammation
XX      CC      such as rheumatoid arthritis. In situ generation of the targeting
XX      CC      antibody increases selectivity, reducing side effects at normal tissue.
XX      CC      The method is applicable to any antibody-directed enzyme prodng therapy
XX      CC      system.
XX      Sequence 843 BP: 197 A; 231 C; 223 G; 192 T; 0 other;

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Query Match      53.8%; Score 489; DB 20; Length 843;
Best Local Similarity 77.6%; Pred. No. 1e-126;
Matches 620; Conservative 0; Mismatches 170; Indels 9; Gaps 2;

```

```

Qy      28  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      28  atgaataaccattgctcactacagcagcgtgctgctgctgctgctgctgctgctg 87
Db      1  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1  atgaataaccattgctcactacagcagcgtgctgctgctgctgctgctgctgctg 60
Qy      88  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      88  atgacgagctgacagcctgacagcagctctggtcgtgaactcgaagacacctgag 147
Db      61  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      61  atgacgagctgacagcctgacagcagctctggtcgtgaactcgaagacacctgag 120
Qy      148  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      148  aagatgctcctgcaagcctgctgctacaccttactaggtacagatgactggtgtaa 207
Db      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      121  aagatgctcctgcaagcctgctgctacaccttactaggtacagatgactggtgtaa 180
Qy      208  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      208  cagagcctgacagcgtctggaatggtatgatacatatctctagcgtggtatct 267
Db      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      181  cagagcctgacagcgtctggaatggtatgatacatatctctagcgtggtatct 240
Qy      268  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      268  aattacaatcgaagttcaagacagcagcattgactacagacaaatctccacagaca 327
Db      241  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      241  gaatagcccgaaagttccgggagcagcacttgactgacagactctccacacaca 300
Qy      328  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      328  gctacatgcaactgacagcctgacatctgagatctgagcttacttactg---tgca 384
Db      301  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301  gctacatgcaactgacagcctgacatctgagatctgagatctgagcttacttactg 360
Qy      385  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      385  agatatatgataatcattacagccttgaactggtggtggtggtggtggtggtggt 444
Db      361  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      361  ctgactatgctggttacttggctatgactggtggtggtggtggtggtggtggtg 420
Qy      445  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      445  tcttaagccaacaacacccaagcttgaagaagttgaatttcaagaagcagcgtagat 504
Db      421  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      421  agctcggtggtggtggtggtc-----ggcggtggtggtggtggtggtggtggt 474
Qy      505  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      505  atcggtcgaactcagcttccacagcaatctgctgcatctccagggaggaagttacca 564
Db      475  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      475  atggtgctcaccacagcttccacagcaatctgctgcatctccagggaggaagttacca 534
Qy      565  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      565  acctgacgtgcccagctcgaagtgtaagttacatgaaactggtaccagacagaatcag 624
Db      535  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      535  acctgacgtgcccagctcgaagtgtaagttacatgaaactggtaccagacagaatcag 594
Qy      625  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      625  tcccccaaaagatgattatgacacatccaactggtcttcggggtccctgctacttc 684

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[illegible]

XX	Anti-EGFR single chain antibody (Clone 11 H 1).
DE	Single chain antibody; antibody; epidermal growth factor receptor;
XX	EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW	assessment; phage antibody library; ss.
XX	
OS	Mus musculus.
XX	
FH	Key
FT	CDS -
FT	/tag= 1..726
FT	/product= a Single-chain Fv, heavy and light chain plus linker.
PB	
PN	WO9525167-A1.
XX	
PD	21-SEP-1995.
PF	05-MAR-1995; 95WO-EP00978.
PR	02-DEC-1994; 94EP-0118970.
PR	17-MAR-1994; 94EP-0104160.
PA	(MERE) MERCK PATENT GMBH.
PI	Aden J, Ansell KH, Bendig MM, Blasco F, Guessow D;
DR	Kettleborough AC, Mitjans F, Pluiats J, Rosell E;
WP:	1995-336972/43.
P-PSDB:	R79872.
PT	Anti-EGFR antibodies and single chain Fv antibody fragments
PT	obtained from phage-antibody libraries, useful for diagnosis and
PT	therapy of tumours
XX	
XX	Claim 4; Page 71-72; 93pp; English.
XX	
CC	Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC	and antibodies constructed from anti-EGFR antibody fragments can be
CC	used for diagnosis of tumours and assessment of tumour growth in
CC	vivo and in vivo. They may also be used in a pharmaceutical
CC	composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC	The antibodies and fragments are derived from mice but are humanised
CC	so as to cause minimum reaction against them. They are produced
CC	using the phage antibody library. (See T04011-T04026 and
CC	R79858-R79873)
SC	Sequence 726 BP; 174 A; 191 C; 206 G; 155 T; 0 other;
Query Match	. 53.5%; Score 486; DB 16; Length 726;
Best Local Similarity	81.2%; Pred. No. 6.5e-126;
Matches 593; Conservative	0; Mismatches 125; Indels 12; Gaps 2
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X	X	D	E	Anti-EGFR single chain antibody (Clone I E 3).
X	X	K	M	Single chain antibody; antibody; epidermal growth factor receptor;
K	M	E	G	R; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
K	M	a	s	sessment; phage antibody library; ss.
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O	S	M	us	musculus.
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F	T	/product=	Single-chain Fv, heavy and light chain	
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P	N	W	09525167-A1.	
X	X	P	N	
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X	X	P	F	16-MAR-1995; 95WO-EP00978.
X	X	P	R	02-DEC-1994; 94EP-0118970.
P	R	17-MAR-1994;	94EP-0104160.	
X	X	(MERE)	MERCK PATENT GMBH.	
P	A	Adan J,	Anseli KH, Bendig MM, Blasco F, Guessow D;	
P	I	Kettlborough AC, Mijtens F, Piulats J, Roselli E;		
X	X	WI.	1995-336972/43.	
D	R	P-PSDB.	R79869.	


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:51:13 ; Search time 56.59 Seconds
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Title: US-09-424-705-1

Perfect score: 909

Sequence: 1 gaattcataaagagagaa.....atcacatcataatcata 909

Scoring table: IDENTITY NUC
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Searched: 280836 seqs, 80580151 residues

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Minimum DB seq length: 0
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Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:*
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Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	529	58.2	720	3	US-08-502-486-10
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4	515.2	56.7	810	2	US-08-652-507-1
5	485.6	53.4	738	2	US-08-553-497A-23
6	483.8	53.2	726	2	US-08-553-497A-25
7	479.6	52.8	732	2	US-08-553-497A-19
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11	397.2	43.7	831	2	US-08-403-853-17
12	393.8	43.3	883	3	US-09-184-658-7
13	379.8	41.8	720	2	US-08-800-198-7
14	379.8	41.8	720	3	US-09-296-595-7
15	369.8	40.7	891	2	US-08-894-922A-9
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17	367.2	40.4	1570	2	US-08-303-569B-6
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20	342.8	37.7	708	2	US-08-190-199A-60
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43	299.8	33.0	384	2	US-08-656-586-1	Sequence 1, Appl
44	299.4	32.9	354	2	US-08-273-146-58	Sequence 58, Appl
45	298.8	32.9	735	4	PCT-US94-14106-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-279-772A-7
; Sequence 7, Application US/08279772A
; Patent No. 6080560
; GENERAL INFORMATION:
; APPLICANT: Russell, David R
; TITLE OF INVENTION: Method for Producing Antibodies in Plant
; TITLE OF INVENTION: Cells
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles and Brady
; STREET: PO Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: United States of America
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,772A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..719
; US-08-279-772A-7

Query Match 58.2%; Score 529; DB 3; Length 719;
Best Local Similarity 85.0%; Pred. No. 6.8e-154;
Matches 621; Conservative 0; Mismatches 95; Indels 15; Gaps 2;
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Db      706  CTGGAGCTCAA 716

RESULT      3
US-08-463-163-2
Patent No. 5696237
GENERAL INFORMATION:
APPLICANT: Fitzgerald, David J.
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pastan, Ira H.
APPLICANT: Waldmann, Thomas A.
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /product= "Anti-Tac(Fv)-pE40"
US-08-463-163-2

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-652-507-1

Query Match 56.7% Score 515.2; DB 2; Length 810;
Best Local Similarity 78.9%; Pred No. 1.3e-149;
Matches 642; Conservative 0; Mismatches 163; Indels 9; Gaps 2;

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256 cgtggttataactaataacaaagttcaagagcaaggccacattgactacaga 315
241 AATGGTGAATACGAATATGCCCGAAGTTCAGGGCAAGGCCACTTTTACTCA 300
316 tctctcagcagcagctacatgtaactgagcagctgacatctbtagacctctg 375
301 TCCCTCCAAACACAGCTCACTGAGCTGACAGCTGACATCTGAGACACTGCG 360
376 tactg---tgcaagatatatgtagtcaatcagcctgtaactcggggccagc 432
361 TATGTGAATGAGGAGGAGCTGCGACTGGCCCTACTACTTTGACTACTGCG 420
433 actctcagcagctcctcagcacaacacaccccaagcttgaagaagtgaa 492
421 ACGGTACCGCTCTCCACG-----GTGAGGCGGCTTCAAGCGGAGTGGCT 474
493 gcaagtgtagatagtgtagtcaactagctcagcagcaatcagctcagcagg 552
475 GCGGATCTCAAAATGTGCTCACCGCTCCACGACATATGCTCATCTCCAGG 534
553 aaggtacacatgacctgctcagctcagcagctcaagtgtatatacagcagc 612
535 AAGGTACACATAACTGCACTGCGACTGCGACTCAAGTGAAGTGAAGTGTG 594
613 aagtcagcagcactccccaagaatgatttatgacacatccaactgcttcgag 672
595 AAGCCAGGCACTTCTCCAAACTCTGATTTATAGCACATCCAACTGGCTTGA 654

673 cctgctcactcagggcgagtggtctgggaaccttactctcacaatcagcgcatg 732
655 CCGTCTCGCTTCACTAGTGGCAGTGTGATCTGGGACCTCTTACTCTCTCA 714
733 gaagctgaagatgctgcacattacttcacagcagtgtagtagtaaccatcag 792
715 GAGGCTGAAGAGTGTCTCCACTTATTAAGGAGTGAAGGAGTGAAGGAGTGA 774
793 ggtcggggacaaagtgtgaataaacgggctg 826
775 GGTGCTGGCACAAGCTGAGCTGAACGGGCGG 808

RESULT 5
US-08-553-497A-23
Sequence 23, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIS, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSON, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PUIGATS, JAUME
TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-BGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MILLEN, WHITE, ZEILAND & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: NO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

```

; ORIGINAL SOURCE:
; ORGANISM: mouse
; STRAIN: Balb/c
; TISSUE TYPE: splenocytes
; IMMEDIATE SOURCE:
; CLONE: 1 E 3 (single-chain Fv, heavy and light chain
; FEATURE: plus linker)
; NAME/KEY: CDS
; LOCATION: 1..738
; US-08-553-497A-23

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Query Match      53.4%; Score 485.6; DB 2; Length 738;
Best Local Similarity 80.8%; Pred. No. 1.7e-140;
Matches 595; Conservative 0; Mismatches 129; Indels 12; Gaps 2;

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QY 95 aggtgcaagctgcagcagctctgggctgaactgcaagacctggggcctcagtgaaagt 154
DB 2 aggtgcaagctgcagcagctctgggctgaactgcaagacctggggcctcagtgaaagt 154
QY 155 cctgcaagctctgctcgaactcttactgagfacaagcagctggggtgtaaacagagggc 214
DB 62 cctgcaagctctgctcgaactcttactgagfacaagcagctggggtgtaaacagagggc 214
QY 215 ctggagcaggtctggaatgagttgatacttaactcctagccgtggtatataactaata 274
DB 122 ctggagcaggtctggaatgagttgatacttaactcctagccgtggtatataactaata 274
QY 275 atcagaagctcagaagcagaagccacattgactacagaacaaatccacagcagcctaca 334
DB 182 atcagaagctcagaagcagaagccacattgactacagaacaaatccacagcagcctaca 334
QY 335 tgcacatgacagcagcctgaactcgaagacctcgaactcgaactcgaactcgaactcga 394
DB 242 tgcacatgacagcagcctgaactcgaagacctcgaactcgaactcgaactcgaactcga 394
QY 395 atgatactcag-----cctgactactggggccaagcagcagcagcagcagcagcagc 448
DB 302 atgatactcag-----cctgactactggggccaagcagcagcagcagcagcagcagc 448
QY 449 cagcaaaaacaaacacacacagcctgaagaagtgaaatlttcagaagcagcagcagcagc 508
DB 362 cagcaaaaacaaacacacacagcctgaagaagtgaaatlttcagaagcagcagcagcagc 508
QY 509 tgcctcactcagctcgaagcaatcagctcagctcgaagcagcagcagcagcagcagcagc 568
DB 422 agctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 568
QY 569 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 628
DB 482 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 628
QY 629 ccaaaagatgattatgacacatccaactggtctcgaagcagcagcagcagcagcagcagc 688
DB 542 ccaaaagatgattatgacacatccaactggtctcgaagcagcagcagcagcagcagcagc 688
QY 689 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 748
DB 602 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 748
QY 749 ccaactattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 802
DB 662 ccaactattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 802
QY 803 caaagtcgaataaa 818
DB 722 CCAAGCTGGAAATPAA 737

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RESULT 6
US-08-553-497A-25
; Sequence 25, Application US/08553497A

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; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTERBROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSEW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PILARIS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ. ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: mouse
; STRAIN: Balb/c
; TISSUE TYPE: splenocytes
; IMMEDIATE SOURCE:
; CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
; FEATURE: linker)
; NAME/KEY: CDS
; LOCATION: 1..726
; US-08-553-497A-25

```

```

Query Match      53.2%; Score 483.8; DB 2; Length 726;
Best Local Similarity 81.0%; Pred. No. 6.1e-140;
Matches 592; Conservative 0; Mismatches 127; Indels 12; Gaps 2;

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Db 242 TGCACCTCAGCAGCTGACATCTGAGGACTCTGCGCTTAATTAATGTCACAGTGGGACT 301
 QY 395 atgatactaacg-----cctgaactactgggccaaggcacaactctcaagtcctcct 448
 Db 302 ATGATTACGACGACGAGTACTTTGACTACTGGGGCCAGGAGCAGCGTACCGTCTCCT 361
 QY 449 cagcaaaaacacacccaagcttgaagaggatgaaatttcagaagcagcgtatgatacg 508
 Db 362 CAGGTGGCGGTGCTCG-----GGCGGTGGTGGTGGTGGTGGCGGAGTATGACATTG 415
 QY 509 tgcatactcaagtcctcagcaatcatgtctcactcctcagggggaaggttacaatgact 568
 Db 416 AGCTCACCCAGCTCCAGCAATATGCTGCAATCTCCAGGGGAGAGGTACCATGACCT 475
 QY 569 gcagtcacagctcaagtgttaagttacatgaactgaactgaactgaactgaactgaactccc 628
 Db 476 GCAGTGCAGCTCAAGTGTAACTTACATGATGATGATGATGATGATGATGATGATGATG 555
 QY 629 ccaaaagatgattatgacacatccaactggtctctcagtcctcctcactcaaggg 688
 Db 536 CCAGACTCCCTGATTTATGACACATCCACACTGCGCTTCTGAGTCCCTGCTTCAGTG 595
 QY 689 gcagtggtctgaggaactctactctcactcactcagggcagggcagggcagggcagggc 748
 Db 596 GCAGTGGGTCTGGACCTTACTCTCTCACAATCAGCCGAATGAGAGGCTGAAGATGCTG 655
 QY 749 ccaactactactcagcagcagctgagtagtaacca-----ttcagctcgcctcgggga 802
 Db 656 CCAGTTATTAATCTCCAGCAGTGTGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 715
 QY 803 caaagttggaataaa 818
 Db 716 CCAAGCTGGAATATA 731

RESULT 8

US-08-553-497A-21
 ; Sequence 21, Application US/08553497A
 ; Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETTLERBOROUGH, C. A.
 APPLICANT: BENDIG, MARY M.
 APPLICANT: ANSEL, KATH H.
 APPLICANT: GUSSON, DETLEF
 APPLICANT: ADAN, JAUME
 APPLICANT: MITJANS, FRANCESC
 APPLICANT: ROSELL, ELISABET
 APPLICANT: BLASCO, FRANCESC
 APPLICANT: PIULATS, JAUME
 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 STREET: 2200 CLARENDON BLVD. SUITE 1400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: US
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,497A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/EP95/00978
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94104160.0

FILING DATE: 17-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94118970.6
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HAWLEY-KING, DIANA
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: MERCK 1726
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 732 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: mouse
 STRAIN: Balb/c
 TISSUE TYPE: splenocytes
 IMMEDIATE SOURCE:
 CLONE: 3 D 3 (single-chain Fv, heavy and light chain)
 CLONE: plus linker)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..732
 US-08-553-497A-21

Query Match 51.9%; Score 471.6; DB 2; Length 732;
 Best Local Similarity 80.7%; Pired. No. 3,6e-136;

Matches 594; Conservative 0; Mismatches 124; Indels 18; Gaps 3;

QY 95 aggtgcagctgcagcagctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 154
 Db 2 AGGTCCACCTGACGACGACTGAGGGGCTGAATGAGGAGCTGGGGCTTCAGTGAATGT 61
 QY 155 cctgcagagctctggtacaccttactagatcacagatgacatggtggtggtggtggtggtggt 214
 Db 62 CCTGCAAGGCTTCGGGCTTACACCTTACACGACGACCTGATGATGATGATGATGATGATGATG 121
 QY 215 ctggaacaggtctggaatgattgatacaatcctcagcgtgtgttataactaata 274
 Db 122 CTGGACAAAGGCTTGAAGTGGATGAGAGTTTATCCACCAAGCGGCGCTACTACTACA 181
 QY 275 atcagaagttcagaagcagaagcagacttgaactaagaacaaatctctcagaagacactaca 334
 Db 182 ATGAGAAATCAAGAGCAGAGCCACACTGACTGACAAATCTCCAGCAGCCTTACA 241
 QY 335 tgcacatgagcagctgacacatcaggaactctgcaactctactactactgcaagaataatg 394
 Db 242 TGCACCTCAGCAGCTGACATCTGAGGACTCTGGGCTATTAATGCTGACGAGTGGGACT 301
 QY 395 atgatactaacg-----cctgaactactgggccaaggcacaactctcaagtcctcct 448
 Db 302 ATGATTACGACGACGAGTACTTTGACTACTGGGGCCAGGAGCAGCGTACCGTCTCCT 361
 QY 449 cagcaaaaacacacccaagcttgaagaggatgaaatttcagaagcagcgtatgatacg 508
 Db 362 CAGGTGGCGGTGCTCG-----GGCGGTGGTGGTGGTGGTGGCGGAGTATGACATTG 415
 QY 509 tgcatactcaagtcctcagcaatcatgtctcactcctcagggggaaggttacaatgact 568
 Db 416 AGCTCACCCAGCTCCAGCAATATGCTGCAATCTCCAGGGGAGAGGTACCATGACCT 475
 QY 569 gcagtcacagctcaagtgttaagttacatgaactgaactgaactgaactgaactgaactccc 628
 Db 476 GCAGTGCAGCTCAAGTGTAACTTACATGATGATGATGATGATGATGATGATGATGATG 555

QY 629 ccaaaagatgatttatgacacatccaactgcttcgtgagctcctgctcaacttcagg 688
 DB 536 CCAGACTCCTGATTATATGACACATCCACCTGCTTGAGTCCCTGTTGCTTACGTG 595
 QY 689 gcagtggtctgagcttactctctcaacatcagcgagctgaggtgaggaatgcctg 748
 DB 596 GCAGTGGCTGTGGAGCTTCTACTCTCACAATCAGCCGAATGAGGCTGAAGATGCTG 655
 QY 749 ccaattattactgcccagcagctgagtagtaaacca-----ttcacgttcgctcgagg 802
 DB 656 CCACCTATTACTGCGCCAGCAGTGGAGTAGTTACCCACCACCTGTACAGCTTCGAGGCGGGA 715
 QY 803 caaagttggaataaa 818
 DB 716 CCAAGCTGGAATATA 731

RESULT 9
 US-553-497A-27
 Sequence 27, Application US/08553497A

Patent No. 5844093
 GENERAL INFORMATION:

APPLICANT: KETTLEBOROUGH, C. A.
 APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KEITH H.
 APPLICANT: GUSLOW, DETLEF

APPLICANT: ADAM, JADME
 APPLICANT: MITJANS, FRANCESCA

APPLICANT: ROSELL, ELISABET
 APPLICANT: BLASCO, FRANCESC

APPLICANT: PIULATS, JADME
 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:

ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
 STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON
 STATE: VA

COUNTRY: US
 ZIP: 22201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,497A

FILING DATE: 17-NOV-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94104160.0
 FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94118970.6

FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA
 REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1726
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:

LENGTH: 726 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: mouse
 STRAIN: Balb/c
 TISSUE TYPE: splenocytes
 IMMEDIATE SOURCE:
 LIBRARY: 7 G 1 (single-chain Fv, heavy, light chain,
 LIBRARY: linker)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..726
 US-08-553-497A-27

Query Match 51.5%; Score 468.4; DB 2; Length 726;
 Best Local Similarity 79.7%; Pred. No. 3.5e-135;
 Matches 582; Conservative 0; Mismatches 136; Indels 12; Gaps 2;

QY 95 aggtgagctgcaagcagctctggtgagctgcaagcctgggctcctgaagatgt 154
 DB 2 AGGTCAAGCTGCGAGCAGTCAAGGCTGAACTGTAAGCTGGGCTTCACTGAACTGT 61

QY 155 cctgcaagctctgctgctacaccttactaggtacacgagctgagctggaagcagc 214
 DB 62 CCGCAAGGCTTCGCGCTACACCTTACCAAGCCTTGGATCAGTGGGAGAGAGG 121

QY 215 ctgcaaggtctgagatgatatcatatcctacccgtggttactactaattaca 274
 DB 122 GCGGCAAGGCTTGAGTGTGATGAGACATTAAATCCAGCAAGGCGCTACTACTATA 181

QY 275 atcgaagctcagaagcaagcccaatgactacagaacaatcctcagcagcactaca 334
 DB 182 ATGAGAAATTCAGAGCAAGGCGCACACTGATGACAAATCTCCACACAGCTTACA 241

QY 335 tgaactgagcagcctgagatctgagagctcgaagcttactactctggaagatatg 394
 DB 242 TCGAACTCAGCAGCTGACATCTGAGGACTGCTGGTCTATTACTGTGCACTCGGACT 301

QY 395 atgatactatcacag-----ccttgactactggtgccaagcacaactctcacagctcct 448
 DB 302 ATGATTACGACGAGCGGTACTTGTACTACTGGGCCAAGGACAGGCTCAGCTTCTCT 361

QY 449 cagccaaacaacacccaagcttgaagaagtgaaatttcagaagaagcgtagatatcg 508
 DB 362 CAGGTGGCGGTGCTC-----GGCGGTGGTGGGTGGGCGCGGATCTGACATTG 415

QY 509 tgcctcagctcagcagcaatcatgtctgcatctcacaagggagaaggtcacacagact 568
 DB 416 AGCTCACCAGCTCTCCACAATCATCTGTGCACTTCACAGGAGAGAGTACACATGACT 475

QY 569 gcagtgccagctcaagtgtaagttacatgaactggttacagcagaagtgaagcactcc 628
 DB 476 GCAGTGACGCTCAAGTGAAGTGAATGATGTACTGTGACAGCAGAAAGAGAGATCTCC 535

QY 629 ccaaaagatgatttatgacacatccaactgcttcgtgagctcctgctcaacttcagg 688
 DB 536 CCAGACTCCTGATTATATGACACATCCACCTGCTTGAGTCCCTGTTGCTTACGTG 595

QY 689 gcagtggtctgagccttactctctcaacatcagcgagctgaggtgaggaatgcctg 748
 DB 596 GCAGTGGCTGTGGAGCTTCTACTCTCACAATCAGCCGAATGAGGCTGAAGATGCTG 655

QY 749 ccaattattactgcccagcagctgagtagtaaacca-----ttcacgttcgctcgagg 802
 DB 656 CCACCTATTACTGCGCCAGCAGTGGAGTAGTTACCCCTGACGTTGCTGGAGCACAAGC 715

QY 809 tgggaataaa 818
 DB 716 TCGAATATAA 725

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 1..819
FEATURE:
NAME/KEY: CDS
LOCATION: 1..819
US 403-853-17

Query Match 43.7%; Score 397.2; DB 2; Length 831;
Best Local Similarity 71.4%; Pred. No. 3.5e-113;
Matches 573; Conservative 0; Mismatches 208; Indels 21; Gaps 3;

QY 28 atgaataccctatcttcacagcagccgctgtgctgtgctgtgcaagcctcagtg 87
DB 1 ATGAATACCTATTCTCTCAAGCAGCCGCTGATTTTACTCTGCTCCCAACACGCG 60

QY 88 atgagcagctgacagctgcaagcagctgtggtgtgcaagcctcagtg 147
DB 61 ATGGCGAGGTGACAGCTGAGCTGGGCTGAACGTGTAAGCTGGGCTGACAGTG 120

QY 148 aagatgtcctcaaggtctgtgtacaccttactaggtacagatgagtggttaaa 207
DB 121 AGGATGCTCTGCAAGCTTCTGCTACACATTTACCAATTAACATGTAAGGTAAGA 180

QY 208 cagaagcctgagcaggtgtgtgaatgtgattgatacatcaatccctgagtgtaact 267
DB 161 CAGTCACTGGACAGGCTGAGTGATTTGGAATTTTATTCACAGAAATGCTACT 240

QY 268 aattcaatcagaagttcaaggaacagccacatgactacacaaatccctcagcaca 327
DB 241 TCCTACATCAAGAGTTCAAAAGCAAGGCCACATGAGTGTGACAAATCTCCACACA 300

QY 328 gctcacaatgacagcagcctgacatctgagagctctgcagtgctatctagtcaaga 387
DB 801 GCCTACATGCACTCAGCAGCTGACATCTGAGACTCTGCGCTATTAATCTGCAAGA 360

QY 388 -----tatatgatgatcatcattacagccttgactactgtgagcgaagcaccactctc 438
DB 361 TCGGGGGGCTCTATATGATACGACGAGGCTTTGACTACTGGGGCCAAAGGACCCAGGCTC 420

QY 439 acagctcctcagcacaac 498
DB 421 ACCGCTCCGGGGGAGGAGTTC-----GGGTGGGGGAGGTTCCGGGGTGGTGTG 471

QY 499 gtatgatcgtgtcactcagctcagctccagaacatcagctcctcagggagagagtc 558
DB 472 TCGGATATGAGCTCAGCAGACTACATCTCCCTGCTGCTCTCTGGAAGACAGAGTC 531

QY 559 accatgacctgagtgacagcagcagcagcagcagcagcagcagcagcagcagcagcag 615
DB 532 ACCATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 591

QY 616 tcaagcagcctcccccacaaagatgattatgacacatccaacactgctcagtgccct 675
DB 592 CCAAGTGAAGCTGTAAGCTCTGATCTACTACATCAAAATTTACACTCAAGATCCCA 651

QY 676 gtcaactcagggagcagtggtgtgtgagccttactctcacaatcagcagcagtgag 735
DB 652 TCAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 711

QY 736 gctgaagatgctgcacattattacttcagcagcagtgagtagtaaccattcagcttcgc 795
DB 712 CAAGAAGATATTGCCACTTCTTTGCCACAGAGATTTTACCTCTCCGTTCAAGTTCGA 771

QY 796 tgggggacacaaagtgtgaataa 817
DB 772 GGGGGGACCAAGCTCGAGATAA 793

RESULT 12
US-09-184-658-7
Sequence 7, Application US/09184658
Patent No. 6030792
GENERAL INFORMATION:
APPLICANT: Otterness, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 883
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 9A4 single
OTHER INFORMATION: chain antibody, VH - VL.
FEATURE:
NAME/KEY: sig.peptide
LOCATION: (29)..(94)
OTHER INFORMATION: Engineered signal peptide in PCANTAB6; Initiator
OTHER INFORMATION: Coding sequence for genetically engineered single
OTHER INFORMATION: chain antibody - 9A4 VH - VL.
US-09-184-658-7

Query Match 43.3%; Score 393.8; DB 3; Length 883;
Best Local Similarity 68.6%; Pred. No. 4.1e-112;
Matches 599; Conservative 0; Mismatches 247; Indels 27; Gaps 3;

QY 15 ggaagaattaacacgaatattctgctcctcagcagcgcgctgtgtctgtcgtgc 74
DB 16 ggaagatttcaacgagtaaaattattatctgcgaattcccttagtggtccctttatgc 75

QY 75 agctcagcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 134
DB 76 ggcacagcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 135

QY 135 tgggagcctcagtgagatgtcctcagcagcagcagcagcagcagcagcagcagcagcagc 194
DB 136 tggagagagacagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 195

QY 195 gcactggtgtaaaacagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 254
DB 196 acaactggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 255

QY 255 ccgtgttatataatataacacagagtcagagtcagagcagcagcagcagcagcagcagcag 314
DB 256 gactgtgtgagcacaacatgtcagatgactcagagcagcagcagcagcagcagcagcagc 315

QY 315 atccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 374

Db 316 ctctgcgcagcactgcctattctgcagatcaacaactcctaataaagaagcaacggtctataca 375

Qy 375 ttactgtgcagaatataatgatgatcaattaaagccttgactactcggggccaagggcacac 433

Db 376 ttctctgtctcagggcggt-----agccttgactactcggggccaagggcacac 423

Qy 435 tctcaacgtctccctccagccaanaacaacccaagccttgaaagaagttaatttcagagc 494

Db 424 tctcaacgtctccctccag-----gtgaagcggtctcaggcggaagtggcagcggtgtg 477

Qy 495 aagcgatagatcgtgtcactactcagctccagcaatcatgtctgcaltccoaagggagaa 554

Db 478 cgagatcgcgaattgttctcacccagctccagtaattcatgtctgcaltccoaagggagaa 537

Qy 555 ggttaaccaatgcctgcagtgccagctcaagtgtgaagttaactatgcacgtgtaccagcaga 614

Db 538 ggtcaaccatgcctgcagtgccagctcaagtgtgaagttaactatgcacgtgtaccagcaga 597

Qy 615 gtcaagcaccctccccaagaatgatattatgcacatcccaactgtgcttgagctcc 674

Db 558 gccaagatccctccccaagaccctccgatccaatgcacatcccaactgtgcttgagctcc 657

Qy 675 tgtcactcagggcgagtggtctgtggaccttactctctcacaatcagcggcatgaa 734

Db 658 tgttcgtctcagtgcggtgtgtcttggaaccttactctctcacaatcagcggcatgaa 717

Qy 725 ggtcgaagaatcctccacttaactctccagcagtggaagtgaaccatccaatggttcg 794

Db 718 ggcgtgaagaatcctccacttaactctcagcagtggaagtgaaccatccaatggttcg 774

Qy 795 ctccggggccaagtttggaataaaccgggc-----tgatctgcaccaactgctatc 845

Db 778 tggagggcaccagctgtgaatcatcagcggccgacatcatcatcaccatccagggcgccg 837

Qy 846 cgaacaaagctgtatctcagaagaagacctaa 878

Db 838 agaacaaaactcatctcagaagaagatctgaa 870

RESULT 13
US-08-800-198-7
Sequence 7, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

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: TELEFAX: 703-243-6410
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 720 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-800-198-7

```

Query Match	41.8%;	Score 379.8;	DB 2;	Length 720;
Best Local Similarity	72.3%;	Pred. No. 7.8e-108;		
Matches 524; Conservative	0;	Mismatches 192;	Indels 9;	Gaps 2;

OY	94	caggtgcagcgcgaagcaatctcggggctgaaacttgccaagacctggggcctcagtgaaatg	153
Db	1	CAGGTGCAGCTGCAGAGACTCTGGGGCTGAACTGGCCAAACCTGGGGCTCAGTGAAGATG	60
OY	154	tccctgcaagsgctctcgtgataaccttctaagtagtacaagatgcaactcgtggtaaaacagag	213
Db	61	TCCTGCAAGSGCTTCGGCTACACCTTTACTAACTAGTGATGACACTGGTGAGACAGAGG	120
OY	214	ccttgcaagsgctctcgtgaatgtaattggataacttaactcttagccgttggtataactaac	273
Db	121	CCTGCAAGSGCTGCTGTAATGATGGATACACTAACTCAACCTGGTTATACGATTC	180
OY	274	aatcgaagatccaaggaagaagggcaacttggactcagaacaatcctctcagaacagccctac	333
Db	181	AATCAGAAGTTCAAGAGCAAGCAAGCCACATTTGACTCAGACAAATCTCCAGCACAGCTTAC	240
OY	334	atgcaactcgaagcaagccttacaactcgtgaggaactctgagtctactaactctgtgcaagataat	393
Db	241	ATGCAACTGAGCGGGCGCTGACATCTGAGGAGACTCTGAGTATTACTGCTGCAAGAGGGAT	300
OY	394	gatgatcatctacagccttgactactctggggccaagagaccacactcacaagtcctcctcagcc	453
Db	301	TACTACGCGCTACGAACCTTGGCTTACTGGGGCCAAAGGACACAGGTCACGTTTCCCTGGGC	360
OY	454	aaaacaaccccagaagcttgaagaagtgaaatttccagaagaagcgttagatactgctc	513
Db	361	GGTGGCGGTTCTCTTCTGATGGGGTGCGCCGGGTGGCGGTTCTGACATCCACTGG	414
OY	514	aactcagctccagaatcatctctgcactctccaggagggaagaagctcaccaatgacctgagct	573
Db	415	AOCGAGTCTCCAGCATCTCTCTCTGTAGTGTCCAGAGAAAGATCAACTTTCTCCTGGAGG	474
OY	574	gcccagctcaag---tgtaagttacatgaaacttgtaaccagcagaagtcaggcaactcccc	630
Db	475	GCCAGTCCAGACATTTGGCACAAATATACACTGATATGACGAAGAAACAAATGGTTCCCA	534
OY	631	aaaagaatgattttagacacatcccaactcgtcctctgagctgcctctgtaactctcaagggc	690
Db	535	AGGCTTCTCATTAAGATAGCTTCTGAGCTATCTCTGTGGATCCCTTCCAGGTTTAAAGTGC	594
OY	691	agtgagctcgggaacctcttactctctcaacaacgaacggcagctgtagagcttgagctgcgc	750
Db	595	AGTGAGTCAAGGACAGATTTTACTCTTAAGCATCAACAGTGTGGAGTGTGGACAGATATTGCA	654
OY	751	actatactacgcagcagctgtagtagtaaccacttcaactcaagcttcgagcttcggggacaagctg	810
Db	655	GATTATTACTCTCAACAAGATGATAGCTGGCCAAACGCTTCGGTCTGCGGACAAGCTC	714
OY	811	gaat 815	
Db	715	GAGAT 719	

RESULT 14
US-09-296-595-7
; Sequence 7, Application US/09296595A

Patent No. 6129915
 GENERAL INFORMATION:
 APPLICANT: WELS, WINFRIED S.
 APPLICANT: SCHMIDT, MATTHIAS
 APPLICANT: VAKALOPOULOU, EVANGELIA
 APPLICANT: SCHNEIDER, DOUGLAS
 TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
 FILE REFERENCE: SCH-1576 D1
 CURRENT APPLICATION NUMBER: US/09/296,595A
 CURRENT FILING DATE: 1999-04-23
 EARLIER APPLICATION NUMBER: 08/800,198
 EARLIER FILING DATE: 1997-02-13
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 7
 LENGTH: 720
 TYPE: DNA
 ORGANISM: Murine sp.
 US-09-296-595-7

Query Match 41.8%; Score 379.8; DB 3; Length 720;
 Best Local Similarity 72.3%; Pred. No. 7.8e-108;
 Matches 524; Conservative 0; Mismatches 192; Indels 9; Gaps 2;

QY 94 caggtgcagctgcagcagctgcggtgcgaactgcgcaagaacctggtggtcctcaatgaatg 153
 DB 1 caggtgcagctgcagcagctgcggtgcgaactgcgcaagaacctggtggtcctcaatgaatg 60
 QY 154 tctctcaagctctgcgtgcacaccttactagttacacgacgtacacgtggttaaacgaag 213
 DB 61 tctctcaagctctgcgtgcacaccttactagttacacgacgtacacgtggttaaacgaag 120
 QY 214 cctggacaggtgctggaatgattgatatacattacccagcgtgtgatactaatlac 273
 DB 121 cctggacaggtgctggaatgattgatatacattacccagcgtgtgatactaatlac 180
 QY 274 aatcagaatctcaagaagcagcaccatctgactacagacacaaatcctccacagcactac 333
 DB 181 aatcagaatctcaagaagcagcaccatctgactacagacacaaatcctccacagcactac 240
 QY 334 atgcagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 393
 DB 241 atgcagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 QY 394 gatgatcatatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 453
 DB 301 tactacgctacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
 QY 454 aaaaacacaccccaagcttgaagaagttgaaatttcagaagcagcagcagcagcagcagc 513
 DB 361 ggtggcggttc-----tggtggcggttcggttcggttcggttcggttcggttcggttc 414
 QY 514 actcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 573
 DB 415 acccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 474
 QY 574 gccagctcaag---tgtaagtacatgaaactgtaccagcagcagcagcagcagcagcagc 630
 DB 475 gccagctcaagatctggcacaataacacgtgtacacagaagaacaatggttcctca 534
 QY 631 aaaaatgataltatgaac 690
 DB 535 aggcctcctcaataagatgctctcgtgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 594
 QY 651 agtgggtctgggaacctctactctctcacaacacagcagcagcagcagcagcagcagcagc 750
 DB 595 agtgggtctgggaacctctactctctcacaacacagcagcagcagcagcagcagcagcagc 654
 QY 751 acttcttactgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 810
 DB 655 gattatctctgcacaaagatgatagtcgtgcacacacagcagcagcagcagcagcagcagc 714

QY 811 gaact 815
 DB 715 gagat 719

RESULT 15

US-08-894-922A-9

Sequence 9, Application US/08894922A

Patent No. 5863765

GENERAL INFORMATION:

APPLICANT: BERRY, Mark John

APPLICANT: DAVIS, Paul James

APPLICANT: VAN DER LOOT, Cornelius P.E.

APPLICANT: WHITEHAM, Garry Clark

TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,922A

FILING DATE: 03-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9504344.4

FILING DATE: 03-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/00468

FILING DATE: 01-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kokulis, Paul K.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 60113/241261

TELEPHONE: (202)-861-3503

TELEFAX: (202)-822-0944

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 891 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA

US-08-894-922A-9

Query Match 40.7%; Score 369.8; DB 2; Length 891;
 Best Local Similarity 69.8%; Pred. No. 1.1e-104;
 Matches 588; Conservative 0; Mismatches 192; Indels 63; Gaps 4;

QY 2 aattcaataaagaagaaataaaccatgaataaactattgctcctcagcagcagcagcagcagc 61
 DB 14 AATTCTATTTCAGAGAGACATGATGAAATGAAATGCTATTGCTTGGGAGGAGCGCTGGAT 73
 QY 62 tgcctgctgctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 121
 DB 74 TCTTATTACTCCCTGCCACACCGCCATGCGCCAGGTGACGTGCAAGCTGTGGGGCTG 133
 QY 122 aactggcaagactggggtcctcagtgaaatgttctctgcaaggtctctggtacacattta 181
 DB 134 AACTGGTGAAGCTGGGCTTCTGTGAAGCTGCTGCAAGGCTTCCGACTACACTTCA 193
 QY 182 ctaggtaacagatgactggtgtaaaacagaggtcctggacaggtcttgtaattgattgatt 241

D	194	CCAGTATTATGGATGACACTGGGTGTAAGCAGAGGCGCTGGACCAAGGCGTTGAGTGGATTGGAG	253
OY	242	acataatcctcctgacccguygttatacctaataaactcagaagttcagaagaccacat	301
D	254	AGATTAAATCCTACCAACGCGTGTGCTATTATTCAAATGGAAGTTCCAAAGCAAGGCCACAC	313
OY	302	tgcatacagacaanaatccctccagacacagcctacacatgcacatcagagagagcctgaactcagag	361
D	314	TGACTGTGAGACAAATCTTCCACGTCACAGCCTACATGCAAGCTCAGCAGCCTACATCTGAGG	373
OY	362	actcctgcagttcattactctgctgcaagataatataatgataatgataatcattacagccttgcactg	421
D	374	ACTCTGCGCGTCTATTACTGTGTCAAGACGGTATG-----GTAACTCCTTGTGACTGAGG	427
OY	422	gcccaagagcacactcctcagctccctccagccaagaacaaacacaccacccaagcttgaagaagct	481
D	428	GCCAAAGGACCAACGCGTACCGCTCTCTCCAGCAATGATGATAA-----	468
OY	482	aatttcagaagcacagcgtgaataatcgtgtgcactcagctcctccagcaatcatgtctgcacat	541
D	469	-----AGGGACATCATGACGTCACCCAGTCTCCAGATTCTTTGGCTGTGT	511
OY	542	ctccaggggagaagtgtaaccatacgtacgtccagtgccagctcaagtga-----	588
D	512	CTCTAAGGCGCAAGGCGCCACCATATCTCCGACAGAGCCACTGAAAGCTTGATAGTTATGGCA	571
OY	589	-agttacatgaactgctgacagcagagaaagtaagcaactcccccnaaagaatgattatg	646
D	572	ATAGTTTATATGCACTGTGACACGACGAAACCAGACAGCACCAACCCAACTCCTATCTATC	631
OY	647	acacatccaacatgctcttgcagagtcctctgtcactccttcagagggcagtggtctgcagact	706
D	632	GTGCTATCCAACTGTAATCTGTGGCATTTCTTGCGCAGAGTCAAGTGCACATGGCGCTTAGGCAC	691
OY	707	cttactctctacacatacagcgagcagatgaagctgaagtgctgcactataactatcgcagc	766
D	692	ACTTCACCCCTACCATTTBATCTCTGTGAGGCGTGAATGATGTGTGCACCTATTATATGTCAAC	751
OY	767	agtg-----gagtagtaacccattacacgtctcgcgtctcggcgagacaagaatltgaaataaac	820
D	752	AAAGATGATGATATCCGATCATGTACAGCTGCGAGGGGGGACCAACCTCGAGATCAAC	811
OY	821	ggg 823	
D	812	ggg 814	

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